Clustal W(1.4) multiple sequence alignment

4 Sequences Aligned.   Alignment Score = 12736
Gaps Inserted = 4   Conserved Identities = 308

Pairwise Alignment Mode: Slow   FIGURE 1
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Similarity Matrix: blosum

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 0.1
    Delay Divergent = 40%   Gap Distance = 8
    Similarity Matrix: blosum

Processing time: 14.5 seconds


```
con3707.pep     1 MDQYCILGRIGEGAHGIVFKAKHVEPRVGWQCLPSILQTGEIVALKKVAL  50
con3705.pep     1 MDQYCILGRIGEGAHGIVFKAKHVEPRVGWQCLPSILQTGEIVALKKVAL  50
con3703.pep     1 MDQYCILGRIGEGAHGIVFKAKHVET-------------GEIVALKKVAL  37
con3702.pep     1 MDQYCILGRIGEGAHGIVFKAKHVET-------------GEIVALKKVAL  37
                  ************************             **********


con3707.pep    51 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD 100
con3705.pep    51 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD 100
con3703.pep    38 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD  87
con3702.pep    38 RRLEDGFPNQALREIKALQEMEDNQYVVQLKAVFPHGGGFVLAFEFMLSD  87
                  *************************************************


con3707.pep   101 LAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 150
con3705.pep   101 LAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 150
con3703.pep    88 LAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 137
con3702.pep    88 LAEVVRHAQRPLAQAQVKSYLQMLLKGVAFCHANNIVHRDLKPANLLISA 137
                  *************************************************


con3707.pep   151 SGQLKIADFGLARVFSPDGSRLYTHQVATRWYRAPELLYGARQYDQGVDL 200
con3705.pep   151 SGQLKIADFGLARVFSPDGSRLYTHQVATRWYRAPELLYGARQYDQGVDL 200
con3703.pep   138 SGQLKIADFGLARVFSPDGSRLYTHQVATR------------------- 167
con3702.pep   138 SGQLKIADFGLARVFSPDGSRLYTHQVATRWYRAPELLYGARQYDQGVDL 187
                  *****************************


con3707.pep   201 WSVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWPELTELPDY 250
con3705.pep   201 WSVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWP-------- 242
con3703.pep   168 -SVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWPELTELPDY 216
con3702.pep   188 WSVGCIMGELLNGSPLFPGKNDIEQLCYVLRILGTPNPQVWPELTELPDY 237
                   *****************************************


con3707.pep   251 NKISFKEQVPMPLEEVLPDVSPQALDLLGQFLLYPPHQRIAASKALLHQY 300
con3705.pep   243 ------EQVPMPLEEVLPDVSPQALDLLGQFLLYPPHQRIAASKALLHQY 286
con3703.pep   217 NKISLKEQVPMPLEEVLPDVSPQALDLLGQFLLYPPHQRIAASKALLHQY 266
con3702.pep   238 NKISFKEQVPMPLEEVLPDVSPQALDLLGQFLLYPPHQRIAASKALLHQY 287
                        *****************************************


con3707.pep   301 FFTAPLPAHPSELPVPQRLGGPAPKAHPGPPHIHDFHVDRPLEESLLNPE 350
con3705.pep   287 FFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRPLEESLLNPE 336
con3703.pep   267 FFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRPLEESLLNPE 316
con3702.pep   288 FFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIHDFHVDRPLEESLLNPE 337
                  ************** ***********************************


con3707.pep   351 LIRPFILEG 359
con3705.pep   337 LIRPFILEG 345
con3703.pep   317 LIRPFILER 325
con3702.pep   338 LIRPFILER 346
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Clustal W(1.4) multiple sequence alignment

4 Sequences Aligned.   Alignment Score = 42511
Gaps Inserted = 4   Conserved Identities = 932

Pairwise Alignment Mode: Slow   FIGURE 2
Pairwise Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 5.0

Multiple Alignment Parameters:
    Open Gap Penalty = 10.0   Extend Gap Penalty = 5.0
    Delay Divergent = 40%   Transitions: Weighted

Processing time: 107.3 seconds


```
con3702.seq    1                     ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG   38
con3703.seq    1 GGACCTTCTAGAATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG   50
con3707.seq    1                     ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG   38
con3705.seq    1                     ATGGACCAGTACTGCATCCTGGGCCGCATCGGGGAGGG   38
                                     **************************************


con3702.seq   39 CGCCCACGGCATCGTCTTCAAGGCCAAGCACGTGGAG-------------   75
con3703.seq   51 CGCCCACGGCATCGTCTTCAAGGCCAAGCACGTGGAG-------------   87
con3707.seq   39 CGCCCACGGCATCGTCTTCAAGGCCAAGCACGTGGAGCCGAGGGTGGGCT   88
con3705.seq   39 CGCCCACGGCATCGTCTTCAAGGCCAAGCACGTGGAGCCGAGGGTGGGCT   88
                 *************************************


con3702.seq   76 -------------------------ACTGGCGAGATAGTTGCCCTCAAG    99
con3703.seq   88 -------------------------ACTGGCGAGATAGTTGCCCTCAAG   111
con3707.seq   89 GGCAGTGTCTGCCTTCTATCCTGCAGACTGGCGAGATAGTTGCCCTCAAG   138
con3705.seq   89 GGCAGTGTCTGCCTTCTATCCTGCAGACTGGCGAGATAGTTGCCCTCAAG   138
                                          *************************


con3702.seq  100 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG   149
con3703.seq  112 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG   161
con3707.seq  139 AAGGTGGCCCTAAGGCGGTTGGAAGACGGCTTCCCTAACCAGGCCCTGCG   188
con3705.seq  139 AAGGTGGCCCTAAGGCGGTTGGAGGACGGCTTCCCTAACCAGGCCCTGCG   188
                 ***********************  *************************


con3702.seq  150 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC   199
con3703.seq  162 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC   211
con3707.seq  189 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC   238
con3705.seq  189 GGAGATTAAGGCTCTGCAGGAGATGGAGGACAATCAGTATGTGGTACAAC   238
                 *************************************************


con3702.seq  200 TGAAGGCTGTGTTCCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC   249
con3703.seq  212 TGAAGGCTGTGTTCCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC   261
con3707.seq  239 TGAAGGCTGTGTTCCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC   288
con3705.seq  239 TGAAGGCTGTGTTCCCACACGGTGGAGGCTTTGTGCTGGCCTTTGAGTTC   288
                 *************************************************


con3702.seq  250 ATGCTGTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCGCTAGC   299
con3703.seq  262 ATGCTGTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC   311
con3707.seq  289 ATGCTGTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC   338
con3705.seq  289 ATGCTGTCGGATCTGGCCGAGGTGGTGCGCCATGCCCAGAGGCCACTAGC   338
                 ********************************************    ***


con3702.seq  300 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTCGCCT   349
con3703.seq  312 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTCGCCT   361
con3707.seq  339 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTCGCCT   388
con3705.seq  339 CCAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTCGCCT   388
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*************************************************

con3702.seq  350 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG  399
con3703.seq  362 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG  411
con3707.seq  389 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG  438
con3705.seq  389 TCTGCCATGCCAACAACATTGTACATCGGGACCTGAAACCTGCCAACCTG  438
                 *************************************************
                                                               --

con3702.seq  400 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG  449
con3703.seq  412 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG  461
con3707.seq  439 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG  488
con3705.seq  439 CTCATCAGCGCCTCAGGCCAGCTCAAGATAGCGGACTTTGGCCTGGCTCG  488
                 *************************************************

con3702.seq  450 AGTCTTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGGTGGCCACCA  499
con3703.seq  462 AGTCTTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGGTGGCCACCA  511
con3707.seq  489 AGTCTTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGGTGGCCACCA  538
con3705.seq  489 AGTCTTTTCCCCAGACGGCAGCCGCCTCTACACACACCAGGTGGCCACCA  538
                 *************************************************

con3702.seq  500 GGTGGTACCGAGCCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG  549
con3703.seq  512 GGT-----------------------------------------------  514
con3707.seq  539 GGTGGTACCGAGCCCCCGAGCTCCTGTATGGCGCCCGCCAGTATGACCAG  588
con3705.seq  539 GGTGGTACCGAGCCCCCGAGCTCCTGTATGGTGCCCGCCAGTATGACCAG  588
                 ***

con3702.seq  550 GGCGTCGATCTGTGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG  599
con3703.seq  515 ----------------CTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG  548
con3707.seq  589 GGCGTCGATCTGTGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG  638
con3705.seq  589 GGCGTCGATCTGTGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGG  638
                           *************************************

con3702.seq  600 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC  649
con3703.seq  549 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC  598
con3707.seq  639 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC  688
con3705.seq  639 GTCCCCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGC  688
                 *************************************************

con3702.seq  650 TTCGCATCTTGGGCACCCCAAACCCTCAAGTCTGGCCGGAGCTCACTGAG  699
con3703.seq  599 TTCGCATCTTGGGCACCCCAAACCCTCAAGTCTGGCCGGAGCTCACTGAG  648
con3707.seq  689 TTCGCATCTTGGGCACCCCAAACCCTCAAGTCTGGCCGGAGCTCACTGAG  738
con3705.seq  689 TTCGCATCTTGGGCACCCCAAACCCTCAAGTCTGGCCGGAGC--------  730
                 ******************************************

con3702.seq  700 CTGCCGGACTACAACAAGATCTCCTTTAAGGAGCAGGTGCCCATGCCCCT  749
con3703.seq  649 CTGCCGGACTACAACAAGATCTCCCTTAAGGAGCAGGTGCCCATGCCCCT  698
con3707.seq  739 CTGCCGGACTACAACAAGATCTCCTTTAAGGAGCAGGTGCCCATGCCCCT  788
con3705.seq  731 -------------------------------AGGTGCCCATGCCCCT  746
                                               ***************

con3702.seq  750 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC  799
con3703.seq  699 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC  748
con3707.seq  789 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC  838
con3705.seq  747 GGAGGAGGTGCTGCCTGACGTCTCTCCCCAGGCATTGGATCTGCTGGGTC  796
                 *************************************************

con3702.seq  800 AATTCCTTCTCTACCCTCCTCACCAGCGCATCGCAGCTTCCAAGGCTCTC  849
con3703.seq  749 AATTCCTTCTCTACCCTCCTCACCAGCGCATCGCAGCTTCCAAGGCTCTC  798
con3707.seq  839 AATTCCTTCTCTACCCTCCTCACCAGCGCATCGCAGCTTCCAAGGCTCTC  888
con3705.seq  797 AATTCCTTCTCTACCCTCCTCACCAGCGCATCGCAGCTTCCAAGGCTCTC  846
                 *************************************************
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(FIGURE 2 cont)

```
con3702.seq    850 CTCCATCAGTACTTCTTCACAGCTCCCCTGCCTGCCCATCCATCTGAGCT   899
con3703.seq    799 CTCCATCAGTACTTCTTCACAGCTCCCCTGCCTGCCCATCCATCTGAGCT   848
con3707.seq    889 CTCCATCAGTACTTCTTCACAGCTCCCCTGCCTGCCCATCCATCTGAGCT   938
con3705.seq    847 CTCCATCAGTACTTCTTCACAGCTCCCCTGCCTGCCCATCCATCTGAGCT   896
                   **************************************************


con3702.seq    900 GCCGATTCCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC   949
con3703.seq    849 GCCGATTCCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC   898
con3707.seq    939 GCCGGTTCCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC   988
con3705.seq    897 GCCGATTCCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGC   946
                   ****  ********************************************


con3702.seq    950 CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG   999
con3703.seq    899 CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG   948
con3707.seq    989 CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG  1038
con3705.seq    947 CCCCCCACATCCATGACTTCCACGTGGACCGGCCTCTTGAGGAGTCGCTG   996
                   **************************************************


con3702.seq   1000 TTGAACCCAGAGCTGATTCGGCCCTTCATCCTGGAGGGGTGAGGATCCTG  1049
con3703.seq    949 TTGAACCCAGAGCTGATTCGGCCCTTCATCCTGGAGGAGGTGAGGATCCTG   998
con3707.seq   1039 TTGAACCCAGAGCTGATTCGGCCCTTCATCCTGGAGGGGTGAGGATCCTG  1088
con3705.seq    997 TTGAACCCAGAGCTGATTCGGCCCTTCATCCTGGAGGGGTGA         1038
                   ********************************** *****


con3702.seq   1050 AGAA 1053
con3703.seq    999 AGAA 1002
con3707.seq   1089 AGAA 1092
con3705.seq   1039      1038
```